What is claimed is:

1. A method of inferring, with a predetermined level of confidence, a trait of an individual, comprising:

a) contacting a sample comprising nucleic acid molecules of a test individual with hybridizing oligonucleotides,

wherein the hybridizing nucleotides can detect nucleotide occurrences of single nucleotide polymorphisms (SNPs) of a panel of at least about ten ancestry informative markers (AIMs) indicative of a population structure correlated with the trait, and

wherein said contacting is performed under conditions suitable for detecting the nucleotide occurrences of the AIMs of the test individual by the hybridizing oligonucleotides; and

b) identifying, with a predetermined level of confidence, a population structure that correlates with the nucleotide occurrences of the AIMs in the test individual, wherein the population structure correlates with a trait,

thereby inferring, with a predetermined level of confidence, the trait of the individual.

2. The method of claim 1, wherein the panel comprises at least about twenty AIMs.

3. The method of claim 1, wherein the trait comprises biogeographical ancestry (BGA).

4. The method of claim 3, wherein the panel comprises AIMs set forth as SEQ ID NOS:1 to 331.

5. The method of claim 3, wherein the panel comprises AIMs set forth as SEQ ID NOS:1 to 71.

6. The method of claim 3, wherein the panel comprises AIMs set forth as:

SEQ ID NOS:7, 21, 23, 27, 45, 54, 59, 63, and 72 to 152;

SEQ ID NOS:3, 8, 9, 11, 12, 33, 40, 59, 63, and 153 to 239;

SEQ ID NOS:1, 8, 11, 21, 24, 40, 172, and 240 to 331; or

combinations thereof.

7. The method of claim 1, wherein at least one AIM of the panel is not linked to a gene linked to the trait.

8. The method of claim 3, wherein the BGA comprises a proportion of a sub-Saharan African, Native American, IndoEuropean, or East Asian ancestral group, or a combination of said ancestral groups.

9. The method of claim 8, wherein the BGA comprises a proportion of at least three ancestral groups.

10. The method of claim 3, wherein the BGA comprises proportions of at least sub-Saharan African and IndoEuropean ancestral groups; Native American and IndoEuropean ancestral groups; East Asian and Native American ancestral groups; or IndoEuropean and East Asian ancestral groups.

11. The method of claim 3, wherein the BGA comprises proportions of at least Native American, East Asian, and IndoEuropean ancestral groups; or sub-Saharan African, Native American, and IndoEuropean ancestral groups.

12. The method of claim 1, wherein the trait comprises responsiveness of the individual to a drug.

13. The method of claim 12, wherein the drug is a cancer chemotherapeutic agent.

14. The method of claim 12, wherein the drug is a statin.

15. The method of claim 1, wherein the trait comprises susceptibility to a disease.

16. The method of claim 15, wherein the disease has an ethnic predisposition.

17. The method of claim 16, wherein the disease is a cancer, diabetes, or hypertension.

18. The method of claim 17, wherein the cancer is prostate cancer.

19. The method of claim 15, wherein the disease is a neurological disorder.

20. The method of claim 19, wherein the schizophrenia or Parkinson's disease.

21. The method of claim 15, wherein the disease is alcoholism.

22. The method of claim 1, wherein the trait comprises a pigmentation trait.

23. The method of claim 22, wherein the pigmentation trait comprises eye color, skin color, hair color, or a combination thereof.

24. The method of claim 1, further comprising identifying, with a predetermined level of confidence, a sub-population structure of the population structure that correlates with the nucleotide occurrences of the AIMs in the test individual, wherein the sub-population structure correlates with a trait.

25. The method of claim 1, wherein the hybridizing oligonucleotides comprise oligonucleotide primers, said method further comprising contacting the sample with a polymerase, under condition suitable for generation of a primer extension product, wherein determining the nucleotide occurrence of a SNP comprises detecting the presence of the primer extension product.

26. The method of claim 1, wherein the hybridizing oligonucleotides comprise oligonucleotide primers, said method further comprising contacting the sample with a polymerase, under condition suitable for generation of a primer extension product, wherein determining the nucleotide occurrence of a SNP comprises determining the nucleotide sequence of the primer extension product at a position corresponding to the position of the SNP.

27. The method of claim 1, wherein the hybridizing oligonucleotides comprise amplification primer pairs, said method further comprising contacting the sample with a polymerase, under condition suitable for generation of an amplification product, wherein determining the nucleotide occurrence of a SNP comprises detecting the presence of the amplification product.

28. The method of claim 1, wherein the hybridizing oligonucleotides comprise amplification primer pairs, said method further comprising contacting the sample with a polymerase, under condition suitable for generation of an amplification product, wherein determining the nucleotide occurrence of a SNP comprises determining the nucleotide sequence of the amplification product at a position corresponding to the position of the SNP.

29. The method of claim 1, which is performed in a high throughput format.

30. The method of claim 1, which is performed in a multiplex format.

31. A method of estimating, with a predetermined level of confidence, proportional ancestry of at least two ancestral groups of an individual, comprising:

a) contacting a sample comprising nucleic acid molecules of a test individual with hybridizing oligonucleotides,

wherein the hybridizing oligonucleotides can detect nucleotide occurrences of single nucleotide polymorphisms (SNPs) of a panel of at least about ten ancestry informative markers (AIMs) indicative of biogeographical ancestry (BGA) for each ancestral group examined, and

wherein said contacting is under conditions suitable for detecting the nucleotide occurrences of the AIMs of the test individual by the hybridizing oligonucleotides; and

b) identifying, with a predetermined level of confidence, a population structure that correlates with the nucleotide occurrences of the AIMs of each of the ancestral groups examined, wherein the population structure is indicative of proportional ancestry,

thereby estimating, with a predetermined level of confidence, proportional ancestry of the individual.

32. The method of claim 31, wherein the proportional ancestry comprises a proportion of a sub-Saharan African ancestral group, a Native American ancestral group, an IndoEuropean ancestral group, an East Asian ancestral group, or a combination thereof.

33. The method of claim 31, wherein the proportional ancestry comprises proportions of sub-Saharan African and IndoEuropean ancestral groups; Native American and IndoEuropean ancestral groups; East Asian and Native American ancestral groups; or IndoEuropean and East Asian ancestral groups.

34. The method of claim 31, wherein the proportional ancestry comprises proportions of Native American, East Asian, and IndoEuropean ancestral groups; sub-Saharan African, Native American, and IndoEuropean ancestral groups; or sub-Saharan African, Native American, and East Asian ancestral groups.

35. The method of claim 31, wherein the panel for at least one of the ancestral groups comprises AIMs as set forth in SEQ ID NOS:1 to 331.

36. The method of claim 31, wherein the panel for at least one of the ancestral groups comprises AIMs set forth as SEQ ID NOS:1 to 71.

37. The method of claim 31, wherein the panel for at least one of the ancestral groups comprises AIMs set forth as:

SEQ ID NOS:7, 21, 23, 27, 45, 54, 59, 63, and 72 to 152;
SEQ ID NOS:3, 8, 9, 11, 12, 33, 40, 59, 63, and 153 to 239;
SEQ ID NOS:1, 8, 11, 21, 24, 40, 172, and 240 to 331; or
combinations thereof.

38. The method of claim 31, wherein at least one AIM of the panel is not linked to a gene linked to the trait.

39. The method of claim 31, wherein the proportional ancestry comprises proportions of three ancestral groups, and wherein identifying a population structure that correlates with the nucleotide occurrences of the AIMs of the test individual comprises:

performing a likelihood determination for affiliation with each of a sub-Saharan African ancestral group, a Native American ancestral group, an IndoEuropean ancestral group, and an East Asian ancestral group;

thereafter selecting three ancestral groups having a greatest likelihood value;

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure or proportional affiliation that correlates with the nucleotide occurrences of the AIMs of the test individual is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

40. The method of claim 31, wherein the proportional ancestry comprises proportions of three ancestral groups, and wherein identifying a population structure that correlates with the nucleotide occurrences of the AIMs comprises:

performing six two-way comparisons comprising likelihood determinations for affiliation between each group with each other group;

thereafter selecting three ancestral groups having a greatest likelihood value;

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure or proportional affiliation that correlates with the nucleotide occurrences of the AIMs of the test individual is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

41. The method of claim 31, wherein the proportional ancestry comprises proportions of three ancestral groups, and

wherein identifying a population structure that correlates with the nucleotide occurrences of the AIMs of the test individual comprises performing three three-way comparisons among the groups,

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure or proportional affiliation that correlates with the nucleotide occurrences of the AIMs of the test individual is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

42. The method of claim 31, wherein the proportional ancestry comprises proportions of four ancestral groups, and

wherein identifying a population structure that correlates with the nucleotide occurrences of the AIMs of the test individual comprises performing six two-way comparisons, three three-way comparisons, or one four-way comparison among the groups;

determining a likelihood of all possible proportional affiliations among the four ancestral groups having the greatest likelihood value, whereby a population structure or proportional affiliation that correlates with the nucleotide occurrences of the AIMs of the test individual is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

43. The method of claim 40, further comprising generating a graphical representation of the comparison of the three ancestral groups, said graphical representation comprising a triangle with each an ancestral group independently represented by a vertex of the triangle, wherein the maximum likelihood value of proportional affiliation for an individual comprises a point within the triangle.

44. The method of claim 43, wherein the graphical representation further comprises a confidence contour indicating a level of confidence associated with estimating the proportional ancestry.

45. The method of claim 31, further comprising identifying, with a predetermined level of confidence, a sub-population structure of the population structure that correlates with the nucleotide occurrences of the AIMs in the test individual, wherein the sub-population structure correlates with ethnicity of the test individual.

46. The method of claim 45, wherein identifying the subpopulation structure comprises

identifying chromosomes of the test individual that contain the AIMs indicative of an ancestral group of the proportional ancestry of the test individual,

contacting a sample comprising nucleic acid molecules of the test individual with second hybridizing oligonucleotides;

wherein the second hybridizing oligonucleotides can detect nucleotide occurrences of SNPs of a second panel of AIMs, and

wherein the AIMs of the second panel are present on the chromosomes of the test individual that contain the AIMs indicative of the ancestral group of the test individual; and

identifying a sub-population structure that correlates with the nucleotide occurrences of the AIMs of the second panel, wherein the sub-population is indicative of ethnicity of the ancestral group of the test individual.

47. The method of claim 45, wherein the ancestral group is IndoEuropean, and wherein the ethnicity comprises Northern European or Mediterranean.

48. The method of claim 31, further comprising generating an ancestral map of the world, wherein locations of populations having a proportional ancestry corresponding to the proportional ancestry of the test individual are indicated on the ancestral map.

49. The method of claim 48, further comprising

a) overlaying the ancestral map with a genealogical map, wherein the genealogical map indicates locations of populations having geopolitical relevance with respect to the test individual, and

b) statistically combining the information of the ancestral map and genealogical map to obtain a most likely estimate of family history of the test individual.

50. The method of claim 31, wherein identifying a population structure that correlates with the nucleotide occurrences of the AIMs comprises comparing the nucleotide occurrences of the AIMs of the test individual with known proportional ancestries corresponding to nucleotide occurrences of AIMs indicative of BGA.

51. The method of claim 50, wherein the known proportional ancestries corresponding to nucleotide occurrences of AIMs indicative of BGA are contained in a database.

52. The method of claim 51, wherein the comparing is performed using a computer.

53. The method of claim 50, wherein each of the known proportional ancestries corresponding to nucleotide occurrences of AIMs indicative of BGA further comprises of photograph of a person from whom the known proportional ancestry was determined.

54. The method of claim 53, wherein the photograph comprises a digital photograph.

55. The method of claim 54, wherein digital information comprising the digital photograph is contained in a database.

56. The method of claim 55, wherein the digital information in the database is associated with a known proportional ancestry corresponding to nucleotide occurrences of AIMs indicative of BGA of the person in the photograph.

57. The method of claim 51, further comprising identifying a photograph of a person having a proportional ancestry corresponding to the proportional ancestry of the test individual.

58. The method of claim 57, wherein identifying the photograph comprises scanning a database comprising a plurality of files, each file comprising digital information corresponding to a digital photograph of a person having a known proportional ancestry, and identifying at least one photograph of a person having nucleotide occurrences of AIMs indicative of BGA that correspond to the nucleotide occurrences of AIMs indicative of BGA of the test individual.

59. An article of manufacture, comprising at least one photograph of a person having a known proportional ancestry corresponding to a population structure comprising nucleotide occurrences of AIMs indicative of biogeographical ancestry (BGA).

60. The article of claim 59, which is contained in a file.

61. A plurality of files comprising the article of manufacture of claim 59, wherein files of the plurality comprise at least one photograph of a person having a known proportional ancestry corresponding to a population structure comprising nucleotide occurrences of AIMs indicative of BGA.

62. The file of claim 60, which comprises a plurality of photographs, wherein photographs of the plurality comprise a photograph of a person having a known proportional ancestry corresponding to a population structure comprising nucleotide occurrences of AIMs indicative of BGA.

63. The file of claim 62, wherein photographs of the plurality comprise photographs of different persons having the same known proportional ancestries.

64. The file of claim 62, wherein photographs of the plurality comprise photographs of different persons having different known proportional ancestries.

65. The article of manufacture of claim 59, wherein the at least one photograph comprises a digital photograph.

66. The article of manufacture of claim 65, wherein the digital photograph comprises digital information.

67. The article of manufacture of claim 66, wherein the digital information is contained in a database.

68. The article of manufacture of claim 65, comprising a plurality of digital photographs.

69. A plurality of the articles of manufactures of claim 65, comprising at least two digital photographs.

70. The plurality of claim 69, wherein the digital photographs comprise digital information.

71. The plurality of claim 70, wherein the digital information is contained in a database.

72. A kit, comprising a plurality of hybridizing oligonucleotides, which comprise at least fifteen contiguous nucleotides of at least five polynucleotides as set forth in SEQ ID NOS:1 to 331, or polynucleotides complementary thereto.

73. The kit of claim 72, wherein the hybridizing oligonucleotides comprise at least fifteen contiguous nucleotides of at least five polynucleotides as set forth in SEQ ID NOS:1 to 71, or polynucleotides complementary thereto.

74. The kit of claim 72, wherein hybridizing oligonucleotides of the plurality comprise at least one nucleotide corresponding to a position of the polymorphism of the polynucleotide, or polynucleotide complementary thereto.

75. The kit of claim 74, wherein hybridizing oligonucleotides of the plurality comprise nucleotide position 50 of a polynucleotide as set forth in any of SEQ ID NOS:1 to 34, 36 to 49, 52 to 55, or 57 to 98, 100 to 105, 107 to 162, 164 to 331, or a polynucleotide complementary thereto.

76. The kit of claim 72, wherein hybridizing oligonucleotides of the plurality comprise at least one probe, at least one primer, or a combination thereof.

77. The kit of claim 76, comprising at least one amplification primer.

78. The kit of claim 76, comprising at least one amplification primer pair, which comprises a forward primer and a reverse primer.

79. The kit of claim 78, further comprising reagents for performing an amplification reaction using the at least one amplification primer pair.

80. The kit of claim 72, further comprising at least one ancestry informative marker (AIM), wherein the AIM corresponds to a hybridizing oligonucleotide of the plurality.

81. The kit of claim 72, further comprising a detectable label, which can be bound to or incorporated into at least one hybridizing oligonucleotide of the plurality.

82. The kit of claim 72, wherein hybridizing oligonucleotides of the plurality are detectably labeled.